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=> d his

     (FILE 'HOME' ENTERED AT 15:12:23 ON 11 MAR 2004)

     FILE 'REGISTRY' ENTERED AT 15:14:04 ON 11 MAR 2004
L1             1 S 9030-45-9/RN

     FILE 'HCAPLUS' ENTERED AT 15:14:12 ON 11 MAR 2004

     FILE 'REGISTRY' ENTERED AT 15:17:14 ON 11 MAR 2004
L2             1 S 3416-24-8/RN

     FILE 'HCAPLUS' ENTERED AT 15:17:22 ON 11 MAR 2004

     FILE 'REGISTRY' ENTERED AT 15:17:33 ON 11 MAR 2004
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L3           SEL L1 1- CHEM :      18 TERMS
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L4           516 S L3

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     FILE 'HCAPLUS' ENTERED AT 15:17:38 ON 11 MAR 2004
L6         21205 S L5
L7           297 S L6 (L) L4
L8            54 S L7 (L) (MICROORGANSIM OR MICRO? OR BACTER? OR EUBACTER?)
L9            31 S L8 AND PD<19970114
L10           30 S L9 AND PD<19960114
L11           16 S L10 AND (GENET? OR MUT? OR MODIF? OR RECOMB?)
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=> d ibib ab 1-16

L11 ANSWER 1 OF 16 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1996:326591 HCAPLUS
DOCUMENT NUMBER: 125:50553
TITLE: Thermoregulation of kpsF, the first region 1 gene in the kps locus for polysialic acid biosynthesis in Escherichia coli K1
AUTHOR(S): Cieslewicz, Michael; Vimr, Eric
CORPORATE SOURCE: Dep. Veterinary Pathobiology, Univ. Illinois, Urbana, IL, 61801, USA
SOURCE: Journal of Bacteriology (**1996**), 178(11), 3212-3220
CODEN: JOBAAY; ISSN: 0021-9193
PUBLISHER: American Society for Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The kps locus for biosynthesis of the capsular polysialic acid virulence factor in Escherichia coli K1 contains at least two convergently transcribed operons, designated region 1 and regions 2 plus 3. On the basis of DNA sequence anal., kpsF appeared to be a good candidate for the first gene of region 1 (M. J. Cieslewicz, S. M. Steenbergern, and E. R. Vimr, J. **Bacteriol**. 175:8018-8023, 1993). A preliminary indication that kpsF is required for capsule prodn. is the capsule-neg. phenotype of an aphT insertion in the chromosomal copy of kpsF. The present communication describes the isolation and phenotypic characterization of this **mutant**. Although transcription through kpsF was required for capsule prodn., complementation anal. failed to indicate a clear requirement for the KpsF polypeptide. However, since E. coli contains at least two other open reading frames that could code for homologs of KpsF, the apparent dispensability of KpsF remains provisional. DNA sequence anal. of 1,100 bp upstream from the kpsF translational start site did not reveal any open reading frames longer than 174 nucleotides, consistent with kpsF being the first gene of region 1. Since kpsF appeared to be the first gene of a region whose gene products are required for polysialic acid transport and because capsule prodn. is known to be thermoregulated, primer extension analyses were carried out with total RNA isolated from cells grown at permissive (37.degree.C) and nonpermissive (20.degree.C) temps. The results revealed a potentially complex kpsF promoter-like region that was transcriptionally silent at the nonpermissive temp., suggesting that thermoregulation of region 1 may be exerted through variations in kpsF expression. Addnl. evidence supporting this conclusion was obtained by demonstrating the effects of temp. on expression of the gene kpsE, immediately downstream of kpsF. Chloramphenicol acetyltransferase assays were carried out with constructs contg. the kpsF 5' untranslated region fused to a promoterless cat cassette, providing further evidence that kpsF is thermoregulated. Although the function of KpsF is unclear, primary structure anal. indicated two motifs commonly obsd. in regulatory proteins and homol. with **glucosamine synthase** from Rhizobium meliloti.

L11 ANSWER 2 OF 16 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1996:276737 HCAPLUS
DOCUMENT NUMBER: 124:336251
TITLE: Purification and characterization of glucosamine-6-P synthase from Saccharomyces cerevisiae
AUTHOR(S): Milewski, Slawomir; Smith, Rachel J.; Brown, Alistair J. P.; Gooday, Graham W.
CORPORATE SOURCE: Department Pharmaceutical Technology and Biochemistry, Technical University Gdansk, Gdansk, 80-952, Pol.
SOURCE: Advances in Chitin Science (**1996**), 1, 96-101
CODEN: ACSCFF
PUBLISHER: Jacques Andre
DOCUMENT TYPE: Journal
LANGUAGE: English
AB L-glutamine:D-fructose-6-phosphate amidotransferase (GlcN-6-P synthase) EC 2.6.1.16, an enzyme catalyzing the first committed step in the biosynthetic pathway leading to the chitin precursor - UDP-GlcNAc, was isolated from Saccharomyces cerevisiae. A **genetically**

engineered yeast strain, overexpressing GFA1 gene coding for GlcN-6-P synthase, was used as a rich source of the enzyme. Conditions were found to prevent previously obsd. substantial loss of the enzyme activity during purifn. The proposed purifn. procedure involved: prepn. of crude ext., pptn. with protamine sulfate followed by elution with pyrophosphate buffer, covalent chromatog. on Thiopropyl-Sepharose, ion exchange FPLC on MonoQ and gel filtration FPLC on Superose 6. The whole procedure could be completed in three days and afforded at least 96% pure protein with 47% recovery. The mol. wt. of the enzyme submit was found to be 79.5 kDa, by SDS-PAGE. The native enzyme is expected to be a dimer, as judged from gel filtration. The enzyme was inhibited by UDP-GlcNAc and this inhibition was found to be uncompetitive in respect to D-fructose-6-phosphate and non-competitive in respect to L-glutamine. Several glutamine analogs were tested as inhibitors and inactivators of the enzyme. Kinetic parameters of inhibition and inactivation were detd.

L11 ANSWER 3 OF 16 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1996:227803 HCAPLUS
DOCUMENT NUMBER: 124:334526
TITLE: Isolation and characterization of the GFA1 gene encoding the glutamine:fructose-6-phosphate amidotransferase of Candida albicans
AUTHOR(S): Smith, Rachel J.; Milewski, Slawomir; Brown, Alistair J. P.; Gooday, Graham W.
CORPORATE SOURCE: Molecular & Cell Biology, Univ. Aberdeen, Aberdeen, AB9 1AS, UK
SOURCE: Journal of Bacteriology (**1996**), 178(8), 2320-7
CODEN: JOBAAY; ISSN: 0021-9193
PUBLISHER: American Society for Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English
AB **Glutamine:fructose-6-phosphate amidotransferase** (**glucosamine-6-phosphate synthase**) catalyzes the first step of the hexosamine pathway required for the biosynthesis of cell wall precursors. The Candida albicans GFA1 gene was cloned by complementing a gfa1 **mutation** of Saccharomyces cerevisiae (previously known as gcn1-1; W. L. Whelan and C. E. Ballou, J. **Bacteriol**. 124:1545-1557, 1975). GFA1 encodes a predicted protein of 713 amino acids and is homologous to the corresponding gene from S. cerevisiae (72% identity at the nucleotide sequence level) as well as to the genes encoding **glucosamine-6-phosphate synthases** in **bacteria** and vertebrates. In cell exts., the C. albicans enzyme was 4-fold more sensitive than the S. cerevisiae enzyme to UDP-N-acetylglucosamine (an inhibitor of the mammalian enzyme) and 2.5-fold more sensitive to N3-(4-methoxyfumaroyl)-L-2,3-diaminopropanoic acid (a glutamine analog and specific inhibitor of **glucosamine-6-phosphate synthase**). Cell exts. from the S. cerevisiae gfa1 strain transformed with the C. albicans GFA1 gene exhibited sensitivities to **glucosamine-6-phosphate synthase** inhibitors that were similar to those shown by the C. albicans enzyme. Southern hybridization indicated that a single GFA1 locus exists in the C. albicans genome. Quant. Northern (RNA) anal. showed that the expression of GFA1 in C. albicans is regulated during growth: max. mRNA levels were detected during early log phase. GFA1 mRNA levels increased following induction of the yeast-to-hyphal-form transition, but this was a response to fresh medium rather than to the morphol. change.

L11 ANSWER 4 OF 16 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1994:626134 HCAPLUS
DOCUMENT NUMBER: 121:226134
TITLE: Abnormal **bacteroid** development in nodules induced by a **glucosamine synthase mutant** of Rhizobium leguminosarum
AUTHOR(S): Marie, C.; Plaskitt, K. A.; Downie, J. A.
CORPORATE SOURCE: John Innes Centre, John Innes Institute, Norwich, NR4 7UH, UK

SOURCE: Molecular Plant-Microbe Interactions (**1994**), 7(4), 482-7
CODEN: MPMIEL; ISSN: 0894-0282
DOCUMENT TYPE: Journal
LANGUAGE: English
AB **Mutation** of the chromosomal gene (glmS) encoding **glucosamine synthase** in Rhizobium leguminosarum biovar viciae results in a **mutant** that can induce nodules on peas, but with greatly reduced level of symbiotic nitrogen fixation. Electron **microscopy** of the nodules revealed that infection and release of the glmS **mutant** from infection threads was normal. However, the subsequent development of **bacteroids** was abnormal; **bacteroids** in the mature zone of the nodule were much larger than controls, were abnormally shaped and highly vacuolated, and underwent rapid senescence. It is proposed that expression of nodM (also encoding a **glucosamine synthase**), present on the symbiotic plasmid, enabled the **mutant** to grow in the rhizosphere and within infection threads, but when the **bacteria** were released from infection threads, the nod genes (including nodM) were no longer expressed, resulting in **glucosamine** limitation of the **bacteroids**. Similarly, **glucosamine** limitation in free-living cultures caused a significant redn. in the amt. of cell wall lipopolysaccharide and in qual. changes to the lipopolysaccharide, as revealed by probing with monoclonal antibodies targeted against lipopolysaccharide epitopes.

L11 ANSWER 5 OF 16 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1993:95239 HCAPLUS
DOCUMENT NUMBER: 118:95239
TITLE: Six nodulation genes of nod box locus 4 in Rhizobium meliloti are involved in nodulation signal production: nodM codes for D-glucosamine synthetase
AUTHOR(S): Baev, Nedelcho; Endre, Gabriella; Petrovics, Gyorgy; Banfalvi, Zsofia; Kondorosi, Adam
CORPORATE SOURCE: Inst. Genet., Hung. Acad. Sci., Szeged, H-6701, Hung.
SOURCE: Molecular and General Genetics (**1991**), 228(1-2), 113-24
CODEN: MGGEAE; ISSN: 0026-8925
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The nucleotide sequence of the nod box locus n4 in Rhizobium meliloti was detd. and revealed 6 genes organized in a single transcriptional unit, which are induced in response to a plant signal such as luteolin. **Mutations** in these genes influence the early steps of nodule development on Medicago, but have no detectable effect on Melilotus, another host for R. meliloti. Based on sequence homol., the first open reading frame (ORF) corresponds to the nodM gene and the last to the nodN gene of Rhizobium leguminosarum. The others do not exhibit similarity to any genes sequenced so far, so they were designated as nolF, nolG, nolH, and nolI, resp. The n4 locus, and esp. the nodM and nodN genes, were found to be involved in the prodn. of the root hair deformation (Had) factor. NodM exhibits homol. to amidotransferases, primarily to the D-glucosamine synthetase encoded by the glmS gene of Escherichia coli. In E. coli the regulatory gene nodD together with luteolin was shown to activate nod genes. On this basis nodM was shown to complement an E. coli glmS- **mutation**, indicating that nodM can be considered as a glmS gene under plant signal control. Moreover, exogenously supplied D-glucosamine restored nodulation of Medicago by nodM **mutants**. These data suggest that in addn. to the housekeeping glmS gene of R. meliloti, nodM as a second glmS copy provides glucosamine in sufficient amts. for the synthesis of the Had factor.

L11 ANSWER 6 OF 16 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1993:19069 HCAPLUS
DOCUMENT NUMBER: 118:19069
TITLE: Rhizobium nodM and nodN genes are common nod genes: nodM encodes functions for efficiency of Nod signal production and bacteroid maturation
AUTHOR(S): Baev, Nedelcho; Schultze, Michael; Barlier, Isabelle;

Ha, Dang Cam; Virelizier, Henri; Kondorosi, Eva; Kondorosi, Adam
CORPORATE SOURCE: Inst. Genet., Hung. Acad. Sci., Szeged, H-6701, Hung.
SOURCE: Journal of Bacteriology (**1992**), 174(23), 7555-65
CODEN: JOBAAY; ISSN: 0021-9193
DOCUMENT TYPE: Journal
LANGUAGE: English

AB It has been shown that R. meliloti nodM codes for **glucosamine synthase** and that nodM and nodN **mutants** produce strongly reduced root hair deformation activity and display delayed nodulation of Medicago sativa. Here, it is demonstrated that nodM and nodN genes from R. leguminosarum biovar viciae restore the root hair deformation activity of exudates of the corresponding R. meliloti **mutant** strains. Partial restoration of the nodulation phenotypes of these 2 strains was also obsd. In nodulation assays, galactosamine and N-acetylglucosamine could replace **glucosamine** in the suppression of the R. meliloti nodM **mutation**, although N-acetylglucosamine was less efficient. In nodules induced by nodM **mutants**, the **bacteroids** did not show complete development or were deteriorated, resulting in decreased N2 fixation and, consequently, lower dry wts. of the plants. This **mutant** phenotype could also be suppressed by exogenously supplied **glucosamine**, N-acetylglucosamine, and galactosamine and to a lesser extent by **glucosamine** 6-phosphate, indicating that the nodM **mutant bacteroids** are limited for **glucosamine**. In addn., by using derivs. of the wild type and a nodM **mutant** in which the nod genes are expressed at a high constitutive level, it was shown that the nodM **mutant** produces significantly fewer Nod factors than the wild-type strain but that their chem. structures are unchanged. However, the relative amts. of analogs of the cognate Nod signals were elevated, and this may explain the obsd. host range effects of the nodM **mutation**. These data indicate that both the nodM and nodN genes of the 2 spp. have common functions and confirm that NodM is a **glucosamine synthase** with the biochem. role of providing sufficient amts. of the sugar moiety for the synthesis of the **glucosamine** oligosaccharide signal mols.

L11 ANSWER 7 OF 16 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1992:404039 HCAPLUS
DOCUMENT NUMBER: 117:4039
TITLE: Rhizobium leguminosarum has two glucosamine synthases, GlmS and NodM, required for nodulation and development of nitrogen-fixing nodules
AUTHOR(S): Marie, C.; Barny, M. A.; Downie, J. A.
CORPORATE SOURCE: John Innes Cent., John Innes Inst., Norwich, NR4 7UH, UK
SOURCE: Molecular Microbiology (**1992**), 6(7), 843-51
CODEN: MOMIEE; ISSN: 0950-382X
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The R. leguminosarum nodM gene product shows strong homol. to the Escherichia coli glmS gene product that catalyzes the formation of glucosamine 6-phosphate from fructose 6-phosphate and glutamine. DNA hybridization with nodM indicated that, in addn. to nodM on the symbiotic plasmid, another homologous gene was present elsewhere in the R. leguminosarum genome. A glucosamine-requiring **mutant** was isolated and its auxotrophy could be cor. by two different **genetic** loci. It could grow without glucosamine when the nodM gene on the symbiotic plasmid was induced or if the cloned nodM gene was expressed from a vector promoter. Alternatively, it could be complemented by a second fragment of R. leguminosarum DNA that carries a region homologous to E. coli glmS. Biochem. assays of glucosamine 6-phosphate formation confirmed that the two R. leguminosarum genes nodM and glmS have interchangeable functions. No nodulation of peas or vetch was obsd. when a double nodM glmS **mutant**, and this block occurred at a very early stage since no root-hair deformation or infection threads were seen. Nodulation and root-hair deformation did occur with either the nodM or the glmS **mutant**, showing that the gene products of either of these genes can be involved in the formation of the lipo-oligosaccharide

nodulation signal. However, the glmS **mutant** formed nodules that had greatly reduced nitrogen fixation. Constitutive expression of nodM restored nitrogen fixation to the glmS **mutant**. Therefore the reduced nitrogen fixation probably occurs because glmS is absent and nodM is not normally expressed in nodules and, in the absence of glucosamine precursors, normal bacteroid maturation is blocked.

L11 ANSWER 8 OF 16 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1992:168835 HCAPLUS
DOCUMENT NUMBER: 116:168835
TITLE: N3-Haloacetyl derivatives of L-2,3-diaminopropanoic acid: novel inactivators of glucosamine-6-phosphate synthase
AUTHOR(S): Milewski, Slawomir; Chmara, Henryk; Andruszkiewicz, Ryszard; Borowski, Edward
CORPORATE SOURCE: Dep. Pharm. Technol. Biochem., Tech. Univ. Gdansk, Gdansk, Pol.
SOURCE: Biochimica et Biophysica Acta (**1992**), 1115(3), 225-9
CODEN: BBACAQ; ISSN: 0006-3002
DOCUMENT TYPE: Journal
LANGUAGE: English
AB N3-Haloacetyl derivs. of L-2,3-diaminopropanoic acid, novel glutamine analogs, were shown to be strong inhibitors of **glucosamine-6-phosphate synthase** from **bacteria** and Candida albicans. The inhibition was competitive with respect to glutamine and non-competitive with respect to D-fructose-6-phosphate. In the absence of glutamine, the tested compds. inactivated **glucosamine-6-phosphate synthase** from C. albicans with Kinact = 0.5 .mu.M, 0.55 .mu.M, and 18.5 .mu.M for bromoacetyl-, iodoacetyl- and chloroacetyl- derivs. of L-2,3-diaminopropanoic acid, resp. The inactivation obeyed the criteria for active site-directed **modification**.

L11 ANSWER 9 OF 16 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1990:51966 HCAPLUS
DOCUMENT NUMBER: 112:51966
TITLE: Alternative route for biosynthesis of amino sugars in Escherichia coli K-12 **mutants** by means of a catabolic isomerase
AUTHOR(S): Vogler, Alfried P.; Trentmann, Stefan; Lengeler, Joseph W.
CORPORATE SOURCE: Fachber. Biol./Chem., Univ. Osnabrueck, Osnabrueck, D-4500, Fed. Rep. Ger.
SOURCE: Journal of Bacteriology (**1989**), 171(12), 6586-92
CODEN: JOBAAY; ISSN: 0021-9193
DOCUMENT TYPE: Journal
LANGUAGE: English
AB By inserting a .lambda. placMu **bacteriophage** into gene glmS encoding **glucosamine 6-phosphate synthetase** (GlmS), the key enzyme of amino sugar biosynthesis, a nonreverting **mutant** of E. coli K-12 that was strictly dependent on exogenous N-acetyl-**D-glucosamine** or **D-glucosamine** was generated. Anal. of suppressor **mutations** rendering the **mutant** independent of amino sugar supply revealed that the catabolic enzyme **D-glucosamine**-6-phosphate isomerase (deaminase), encoded by gene nagB of the nag operon, was able to fulfill anabolic functions in amino sugar biosynthesis. The suppressor **mutants** invariably expressed the isomerase constitutively as a result of **mutations** in nagR, the locus for the repressor of the nag regulon. Suppression was also possible by transformation of glmS **mutants** with high-copy-no. plasmids expressing the gene nagB. Efficient suppression of the glmS lesion, however, required **mutations** in a 2nd locus, termed glmX, which has been localized to 26.8 min on the std. E. coli K-12 map. Its possible function in N or cell wall metab. is discussed.

L11 ANSWER 10 OF 16 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 1989:453032 HCAPLUS
DOCUMENT NUMBER: 111:53032
TITLE: Synthesis of N3-fumaroyl-L-2,3-diaminopropionic acid derivatives. Study of their behavior towards the pure **bacterial glucosamine-6-phosphate synthetase**
AUTHOR(S): Kucharczyk, N.; Vermoote, P.; Le Goffic, F.; Badet, B.
CORPORATE SOURCE: Lab. Bio-org. Biotechnol., ENSCP, Paris, 75231, Fr.
SOURCE: Colloque INSERM (**1989**), 174(Forum Pept., 2nd, 1988), 325-31
CODEN: CINMDE; ISSN: 0768-3154
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The behavior of synthetic N3-fumaroyl-L-2,3-diaminopropionic acid derivs. towards the pure glucosamine-6-phosphate synthetase from Escherichia coli has been investigated. The irreversible, glutamine-site directed, inactivation with radiolabeled N3-(4-methoxyfumaroyl)-L-2,3-diaminopropionate assocd. with covalent incorporation of 0.65-0.92 equiv. of inhibitor per enzyme subunit most likely involves the N-terminal cysteine residue. The position of the label in the inhibitor mol. was used to det. the regioselectivity of the nucleophilic attack. The results are consistent with covalent **modification** of the enzyme through direct addn. of the SH nucleophile from the terminal cysteine residue to these Michael acceptors.

L11 ANSWER 11 OF 16 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1988:418147 HCAPLUS
DOCUMENT NUMBER: 109:18147
TITLE: Molecular cloning and overexpression of the glucosamine synthetase gene from Escherichia coli
AUTHOR(S): Dutka-Malen, Sylvie; Mazodier, Philippe; Badet, Bernard
CORPORATE SOURCE: Lab. Bioorg. Biotechnol., ENSCP, Paris, 75231, Fr.
SOURCE: Biochimie (**1988**), 70(2), 287-90
CODEN: BICMBE; ISSN: 0300-9084
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A **recombinant** plasmid carrying a 4.6 kb restriction endonuclease NcoI-ClaI fragment of genomic DNA from E. coli K12 was constructed. This plasmid complements the glmS **mutation**. Subcloning into pUC18 gave plasmid pGM10 encoding the structural gene of glucosamine synthetase, as judged by overexpression of enzyme activity and the isolation in high yield of the pure protein.

L11 ANSWER 12 OF 16 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1986:103246 HCAPLUS
DOCUMENT NUMBER: 104:103246
TITLE: Insertion of transposon Tn7 into the Escherichia coli glmS transcriptional terminator
AUTHOR(S): Gay, Nicholas J.; Tybulewicz, Victor L. J.; Walker, John E.
CORPORATE SOURCE: M.R.C. Lab. Mol. Biol., Cambridge, CB2 2QH, UK
SOURCE: Biochemical Journal (**1986**), 234(1), 111-17
CODEN: BIJOAK; ISSN: 0306-3275
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Transposon Tn7 is unusual, as it transposes at high frequencies from episomal elements to a unique site in the E. coli chromosome. This unique site is within a region of dyad symmetry, the transcriptional terminator of the glmS gene which encodes the glutamine amidotransferase, glucosamine synthetase [9030-45-9]. Transposition of Tn7 abolishes termination of glmS transcription at this site; the transcripts now extend into the left end of Tn7 and terminate at a new site, tm, 127 base pairs from the left end of Tn7. This region of the transposon contains a long open reading frame which encodes a protein sequence that is significantly related to the transposase proteins of the transposable elements IS1 and Tn3. A weak transcript has been identified that emanates from a promoter on the 5' side of this reading frame. This promoter is over-run by glmS transcripts, and so it appears that expression of the Tn7 transposase may

be regulated by promoter occlusion.

L11 ANSWER 13 OF 16 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1985:107210 HCAPLUS
DOCUMENT NUMBER: 102:107210
TITLE: DNA sequence around the Escherichia coli unc operon. Completion of the sequence of a 17 kilobase segment containing asnA, oriC, unc, glmS and phoS
AUTHOR(S): Walker, John E.; Gay, Nicholas J.; Saraste, Matti; Eberle, Alex N.
CORPORATE SOURCE: Lab. Mol. Biol., Med. Res. Counc., Cambridge, CB2 2QH, UK
SOURCE: Biochemical Journal (**1984**), 224(3), 799-815
CODEN: BIJOAK; ISSN: 0306-3275
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The nucleotide sequence is described of a region of the E. coli chromosome extending from oriC to phoS that also includes the loci gid, unc, and glmS. Taken with known sequences for asnA and phoS, this completes the sequence of a segment of .apprx.17 kilobases or 0.4 min of the E. coli genome. Sequences that are probably transcriptional promoters for unc and phoS were detected, and the identity of the unc promoter was confirmed by expts. in vitro with RNA polymerase. Upstream of the promoter sequence is an extensive region that appears to be noncoding. Conserved sequences are found that may serve to conc. RNA polymerase in the vicinity of the unc promoter. Hairpin loop structures resembling known rho-independent transcription termination signals are evident following the unc operon and glmS. The glmS gene encoding glucosamine synthetase [9030-45-9] was identified by homol. with glutamine 5-phosphoribosylpyrophosphate amidotransferase.

L11 ANSWER 14 OF 16 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1984:450787 HCAPLUS
DOCUMENT NUMBER: 101:50787
TITLE: The inactivation of **glucosamine synthetase** from **bacteria** by anticapsin, the C-terminal epoxyamino acid of the antibiotic tetaine
AUTHOR(S): Chmara, Henryk; Zaehner, Hans
CORPORATE SOURCE: Dep. Pharm. Technol. Biochem., Tech. Univ. Gdansk, Gdansk, 80-952, Pol.
SOURCE: Biochimica et Biophysica Acta (**1984**), 787(1), 45-52
CODEN: BBACAQ; ISSN: 0006-3002
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Incubation of anticapsin (I) with purified glucosamine synthetase (EC 5.3.1.19) (II) from Escherichia coli, Pseudomonas aeruginosa, Arthrobacter aurescens, and Bacillus thuringiensis led to the formation of inactive II irreversibly **modified**. The inactivation reaction followed pseudo-1st-order kinetics. The rate of inactivation at various concns. of I exhibited satn. kinetics, implying that I binds reversibly to II prior to inactivation. The detd. Kinact was in the range of 10-5 M (B. thuringiensis) and 10-6 M (E. coli, P. aeruginosa, A. aurescens). The addn. of glutamine protected II from inactivation by I. I was demonstrated to be a mixed type or competitive inhibitor with respect to glutamine with a Ki of 10-6-10-7 M. Reaction of I with the II exhibited the characteristics of affinity labeling of the glutamine-binding site. Chem. **modification** of the II SH group with various reagents, 5,5'-dithiobis(2-nitrobenzoic acid), 6,6'-dithiodinicotinic acid, 1,1'-dithiodiformamidine, NEM, and iodoacetamide, resulted in inactive II.

L11 ANSWER 15 OF 16 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1977:548435 HCAPLUS
DOCUMENT NUMBER: 87:148435
TITLE: Regulation of glucosamine utilization in Staphylococcus aureus and Escherichia coli
AUTHOR(S): Imada, Akira; Nozaki, Yukimasa; Kawashima, Fumiko; Yoneda, Masahiko

CORPORATE SOURCE: Cent. Res. Div., Takeda Chem. Ind., Osaka, Japan
SOURCE: Journal of General Microbiology (**1977**), 100(2), 329-37
CODEN: JGMIAN; ISSN: 0022-1287
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Growth on **glucosamine** (I) of I- or N-acetylglucosamine (II)-requiring **mutants** of S. aureus 209P and E. coli K12 lacking **glucosamine 6-phosphate synthetase** (EC 5.3.1.19), was inhibited by glucose but growth on II was not. Addn. of glucose to **mutant** colonies growing exponentially on I inhibited growth and caused death of **bacteria**, although chloramphenicol prevented death. Glucose markedly inhibited I uptake by S. aureus and E. coli **mutants** whereas II uptake was only slightly inhibited; glucose uptake was not inhibited by either I or II. In I auxotrophs, glucose caused I deficiency which interrupted cell wall synthesis and resulted in some loss of viability in the presence of continued protein synthesis.

L11 ANSWER 16 OF 16 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1971:84319 HCAPLUS
DOCUMENT NUMBER: 74:84319
TITLE: Isolation and characterization of a glucosamine-requiring **mutant** of Escherichia coli K-12 defective in glucosamine-6-phosphate synthetase
AUTHOR(S): Wu, Henry C.; Wu, Theresa C.; Wu, Henry C.
CORPORATE SOURCE: Health Cent., Univ. Connecticut, Farmington, CT, USA
SOURCE: Journal of Bacteriology (**1971**), 105(2), 455-66
CODEN: JOBAAY; ISSN: 0021-9193
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A **mutant** requiring **glucosamine** (I) or N-acetylglucosamine for growth was isolated from E. coli K12. Depriving the **mutant** of **glucosamine** resulted in a rapid loss of viability. When the **mutant** cells were resuspended in broth media contg. 10 sucrose, the rod-shaped cells became spheroplasts. The presence of sucrose, however, did not prevent the cells from losing their viability. The **mutant** was deficient in **glucosamine-6-phosphate synthetase** (EC 2.6.1.16). The activity of the deaminating enzyme, **2-amino-2-deoxy-D-glucose-6-phosphate ketol-isomerase** (EC 5.3.1.10) appeared normal in this **mutant**. The position of the **mutation** was detd. to be at the 74th min of the Taylor and Trotter map, as shown by co-transduction with phoS (90) and ilv (25) by using **bacterio**-phage P1.